

RECEIVED
TECH CENTER 1500/2900
02 APR 24 PM 4:02

Notch (C)	IDEC-SNP	CQNGGTC---D-VGSY-C-CPPGFT	GK---CE-N
<u>10244 (C)</u>	-NECTM---	CQH---C VNT-GSY-CKC-SG--	G--L-C D
80		CRCFPGYT	GKT CSQ D
95	VNECGMKPRP	CQHR C VNTGSKCFCLS	GMLMP D
133	VNSRTCAMIN	CQYS C EDTIEGPQCLCPSS	GLRLAPN
175	IDECASGKVI	CPYNRRG VNTFGSYCKCHIGFE	LQYISGR
220	INECTMDSHT	CSHHANG FNTQGSF CKCKOGYK	GNGRLCS
<u>CD97 (C)</u>	V-EC-SG-Q--C-SS--C	-NTVGSY-CRCRPGW-P-PG-PN---	D
<u>EGF (C)</u>	NSDSECP LSHDGYCLHDGVCMYIEALDKYACNCVVGXI---	GER--CQYRDLKWWELR	

Figure 1

ST

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCTAGT ATAGCTGTGA AGACACAGAA
 SEQ ID NO: 1

AS

GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
 ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
 GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
 CCCC GGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
 CTTTTCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
 CNAGGACATG TGCCATGATA AACTGTCTAGT ATAGCTGTGA AGACACAGAA
 GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGAATCCGCC TGGCCCCAAA
 TGGAAGAGAC TGTCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT
 GTCCCTACAA TCGAAGATGT GTGAACACAT TTGGAAGCTA CTACTGCAAA
 TGTCACATTG GTTTCGAACT GCAATATATC AGTGGACGAT ATGACTGTAT
 AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA
 ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT
 AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA
 AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG
 CTCACAAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGTTACCCCA
 GAACCCACCA GGAATCCTAC CCCTAAGGTG AACTTGCAGC CCTTCAACTA
 TGAAGAGATA GTTTCAGAG GCGGGAAGTC TCATGGAGGT AAAAAAGGGA
 ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA
 GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT
 CCCTAAGGTG AATGAAGCAG GTGAATTCGG CCTGATTCTG GTCCAAAGGA
 AAGCGCTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTTGAC
 TGCAGCTTCA ATCATGGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA
 TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG
 CAGTTCCGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAAACTT
 CTCCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA
 CCGGCTGGCC GGAGACAAAG TCGGGAAACT TCGAGTGTTT GTGAAAAACA
 GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAAAAGTGG
 AAGACAGGGA AAATTCAGTT GTATCAAGGA ACTGATGCTA CCAAAGCAT
 CATTTTTGAA GCAGAACGTG GCAAGGGCAA AACC GGCGAA ATCGCAGTGG
 ATGGCGTCTT GCTTGTTTCA GGCTTATGTC CAGATAGCCT TTTATCTGTG
 GANNCTGAA TGGTACTATC TTTATATTG ACTTTGTATG TCAGTTCCCT
 GGTTTTTTTG ATATTGCATC ATAGGACCTC TGGCATTTTA AAATTACTAG
 CTGAAAAATT G
 SEQ ID NO: 2

FIGURE 2

GWRNSKGVCEATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE
SEQ ID NO:3

AS
GWRNSKGVCEATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP
NGRDCLDIDECASGKVICPYNRRVCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDS
HTCSHHANCFNTQGSFKCKCKQGYKGNLRCSPAIPENSVKEVLRAPGTIKDRIKKLLAH
KNSMKKKAKIKNVTPEPTRTPPKVNLQPFNYEEIVSRGGNSHGGKKGNEEKMKEGLE
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSLKLEHKDLNISVDCSF
NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN
FCLLFDYRLAGDKVGKLRVFKNSNNALAWKTTSEDEKWKTGKIQLYQGTDATKSIIF
EAERGKGKTGEIAVDGVLLVSGLCPSLLSVDDXMVLSLYLTLYVSSLVFLILHHRTSGI
LKLLAEKL
SEQ ID NO:4

FIGURE 3

ACTAGTGATTTCCATCCTAATACGACTCACTATAGGGCTCAGCGGCCCGCCGGGCGAGGTCTGACGGGACAGCACCCGGTA
 ACTCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGGAGGCGGGCTTAGCTGTCTACGGGGTCCGGCGCGGCC
 CTCCGAGGGGGCTCAGGAGGAGGAGGAGGACCCGTGCGAGAAATGCCTTCGCCCTGGAGCTTCGGCTCCCGCTGCTG
 CTCCCTGGGTGGCAGGTGGTTTCGGGAACGGCGCCAGTGAAGGCATACCGGGTTGTAGCATCGGCACGCTCAGCCTGG
 GGTCGTCACTATGGAACTAACTGGCTGTCTACCGGTGGAGAAAGAAACAGCAAGGGAGTCTGTGAAGCTACATGCG
 AACCTGGATGTAAGTTTGGTGAATGAAACCCGGCCATGCCAACACAGATGTGTGAATACACCGGGAAGAACCTGCAGT
 CAAGATGTGAATGAGTGTGAATGAAACCCGGCCATGCCAACACAGATGTGTGAATACACCGGGAAGCTACAAGTCTT
 TTGCCCTCAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAATCTTAGGACATGTGCCATGATAAACTGTCAAGTATA
 GCTGTGAAGACACAGAAAGGGCCACAGTGCCTGTGTCCATCTCAGGACTCGGCCCTGGCCCCAATGGAAGAGACTGT
 CTAGATATTGATGAATGTCCCTCTGGTAAAGTCATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTA
 CTGCAATGTCACTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGACTATGG
 ATAGCCATACGTGCAGCCACCATGCCAAATTTGCTTCAATACCCAAGGGTCTTCAAGTGTAAATGCAAGCAGGGATATAAA
 GGCAATGGACTTCGGTGTCTGCTCAAAAACAGCATGAAAAGAGGCAAAAATTAATAAATGTTACCCAGAACCCACAGCA
 AATCAAGAAGTTGCTGCTCAAAAACAGCATGAAAAGAGGCAAAAATTAATAAATGTTACCCAGAACCCACAGCA
 CTCCTACCCCTAAGGTGAACCTTGACGCCCTTCAACTATGAAGAGATAGTTTCCAGAGCGGGAACTCTCATGGAGGTAAA
 AAAGGAATGAAGAGAAATGAAGAGGGCTTGAGGATGAGAAAGAGAGAAAGCCCTGAAGAAATGACWTAGAGGA
 GCGAAGCCTCGAGGAGATGTGTTTTTCCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCCTGGTCCAAAGGAAAG
 CGCTAACTTCCAACTGGAACATAAAGATTTAAATATCTCGTGTGACTGCACTTCAATCATGGGATCTGTGACTGGA
 CAGGATAGAGAAGATGATTTGACTGGAATCTCTGTGATCAGATAATGCTATTGGCTTCTATATGGCAGTTCCGGCCTT
 GGCAGTCAAGAAGAGACATTTGGCCGATGAAACTTCTCTACCTGACCTGCAACCCCAAGCAACTCTGTGTTGCTCT
 TTGATTACCGGTGGCCGGAGACAAAGTGGAGAACTTCGAGTGTGTTGTGAAAAACAGTAACAATGCCCCCTGGCATGGAG
 AAGACCACGAGTGAGGATGAAAAGTGGAAAGACAGGGAAATTCAGTTGTATCAAGGAACATGATGCTACCAAAAGCATCAT
 TTTTGAAGCAGAACGTGGCAAGGCAAAACCGGGAAATCGCAGTGGATGGCTCTTGTCTGTTTCAGGCTTATGTCAG
 ATAGCCTTTTATCTGTGATGACTGAATGTACTATCTTTATATTGACTTTGTATGTCAGTTCCTCGGTTTTTTTGATA
 TTGSATCATAGGACCTCTGGCATTTTAAATTTACTAAGCTGAAAAATTTGTAATGTACCAACAGAAATTAATTATTTGAAGA
 TGCCTTTMTTGTATAAGATATGCCAATATTGCTTTAAATATCATCACTGTATCTTCTCAGTCAATTTCTGAATCTTTC
 CACATTATATTATAAAATATGGAATGTGAGTTTATCTCCCTCCTCAGTATATCTGATTTGTATAAGTAAGTTGATGA
 GCTTCTCTGCAACATTTCTAGAAAATAGAAAAAGCAGAGAAATGTTTAACTGTTTGTGACTCTTATGATAGTTT
 TGGAACTATGACATCAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAACTTGATATTTAAAT
 TCTTTGTAATAATAATATCCAAATCATCAAAAAA

SEQ ID NO: 5

MPLPWSLALPLLPLWVAGFGNAASARHHGLLASARQPGVCHYGTKLACCYWRNRNSKGVCEATCEPCKFGECVGNKC
 RCFPGYTGKTSQDVNECGMKPRPCQHRVCNTHGSYKFCFLSGHMLMPDATCVNSRTCAMINCOYSCDETEEGPQCLCPS
 SGLRLAPNGRDCLDIDEASGKVICPNRRVCNTHGSYKFCFLSGHMLMPDATCVNSRTCAMINCOYSCDETEEGPQCLCPS
 GSFCKCKQGYKNGLRCSAIPENSUVKVLRAPGTIKDRIKKLLAHKNSMKKAKIKNVTPEPTPTPKVNLQPNFYEE
 IVSRGNSHGGKNGNEEMKEGLEDEKREKALKNDEXEERSLRGDVFPPKVNAGEFGLILVQRKALTSKLEHKDLNISV
 DCSFNHGICDWKQOREDDFDWNPADRDNAIGFYMAVPALAGHKKIDIGRLKLLPDLQPSNFCLLFDYRLAGDKVGLRV
 FVKNSNNALAWKTTSEDEKWKTKIQLYQGTDAKSIIFEAERGKGTGEIAVDGVLLVSLGLCPDLSLLSVDD

SEQ ID NO: 6

FIGURE 4

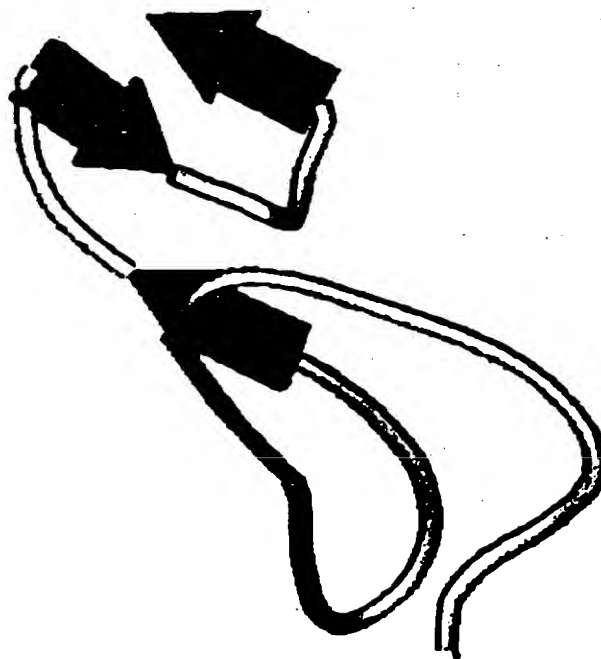
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EGFL6 (221-260 aa)

3D Model

EGF

NMR Structure



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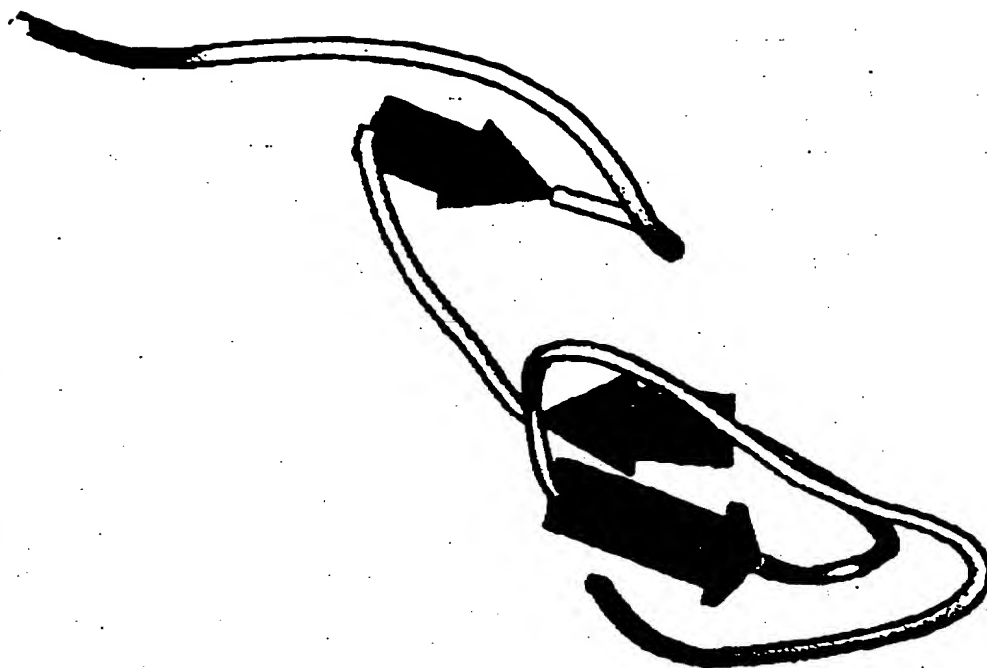


Figure 5